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SEQUENCE LISTING

*REB 51*  
*5*  
*10*  
*15*  
*20*  
*25*  
*30*

(1) GENERAL INFORMATION

(i) APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

(ii) TITLE OF THE INVENTION: GROWTH DIFFERENTIATION FACTOR-12

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Fish & Richardson
- (B) STREET: 4225 Executive Square, Suite 1400
- (C) CITY: La Jolla
- (D) STATE: CA
- (E) COUNTRY: USA
- (F) ZIP: 92037

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: PCT/US95/
- (B) FILING DATE: 12-JUL-1995
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Haile, Ph.D., Lisa A
- (B) REGISTRATION NUMBER: 38,347
- (C) REFERENCE/DOCKET NUMBER: 07265/042WO1 (FD-3830)

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 619-678-5070
- (B) TELEFAX: 619-678-5099
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

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5

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 34 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

10

- (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:
  - (ix) FEATURE:

15

- (A) NAME/KEY: Modified Base  
(B) LOCATION: 12..12  
(D) OTHER INFORMATION: Inosine

20

- (A) NAME/KEY: Modified Base  
(B) LOCATION: 26...26  
(D) OTHER INFORMATION: Inosine

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

25

CCGGAAATTCTG GNTGGMGNVA TGGRTNRTNT AYCC

34

(2) INFORMATION FOR SEO ID NO:2:

30

- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 33 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

35

- (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:

(A) NAME/KEY: Modified Base

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(B) LOCATION: 13...13  
(D) OTHER INFORMATION: Inosine

5

(A) NAME/KEY:Modified Base  
(B) LOCATION: 19...19  
(D) OTHER INFORMATION: Inosine

10

(A) NAME/KEY:Modified Base  
(B) LOCATION: 25...25  
(D) OTHER INFORMATION: Inosine; Inosine also at position  
28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CCGGAATTCCR CANSRCANC YNWCNACNRY CAT

33

(2) INFORMATION FOR SEQ ID NO:3:

15

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:  
(ix) FEATURE:

25

(A) NAME/KEY: Modified Base  
(B) LOCATION: 13...13  
(D) OTHER INFORMATION: Inosine

30

(A) NAME/KEY:Modified Base  
(B) LOCATION: 19...19  
(D) OTHER INFORMATION: Inosine

35

(A) NAME/KEY:Modified Base  
(B) LOCATION: 25...25  
(D) OTHER INFORMATION: Inosine; Inosine also at position  
28

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51

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCGGAATTCTT CANSRCGANT SNYGNACNRY CAT

33

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(iii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

15

(A) NAME/KEY: Modified Base

(B) LOCATION: 13...13

(D) OTHER INFORMATION: Inosine

20

(A) NAME/KEY:Modified Base

(B) LOCATION: 19...19

(D) OTHER INFORMATION: Inosine

25

(A) NAME/KEY:Modified Base

(B) LOCATION: 25...25

(D) OTHER INFORMATION: Inosine; Inosine also at position

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51*  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCGGAATTCCR CANSRCRANT SNWCNACNRY CAT

33

(2) INFORMATION FOR SEQ ID NO:5:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

15 (A) NAME/KEY: Modified Base

(B) LOCATION: 13...13

(D) OTHER INFORMATION: Inosine

20 (A) NAME/KEY:Modified Base

(B) LOCATION: 19...19

(D) OTHER INFORMATION: Inosine

25 (A) NAME/KEY:Modified Base

(B) LOCATION: 25...25

(D) OTHER INFORMATION: Inosine; Inosine also at position

28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CCGGAATTCCR CANSRCRANT SNBTNACNRY CAT

33

(2) INFORMATION FOR SEQ ID NO:6:

30 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

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- (iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:  
(ix) FEATURE:  
5 (A) NAME/KEY: Modified Base  
(B) LOCATION: 13...13  
(D) OTHER INFORMATION: Inosine

- 10 (A) NAME/KEY:Modified Base  
(B) LOCATION: 19...19  
(D) OTHER INFORMATION: Inosine

- 15 (A) NAME/KEY:Modified Base  
(B) LOCATION: 26...25  
(D) OTHER INFORMATION: Inosine; Inosine also at position  
28

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGGAATTCA CANSCRCANG MNYGNACNRY CAT

33

- (2) INFORMATION FOR SEQ ID NO:7:

- 20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- 25 (ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:  
30 (ix) FEATURE:

- (A) NAME/KEY: Modified Base  
(B) LOCATION: 13...13  
(D) OTHER INFORMATION: Inosine

- 35 (A) NAME/KEY:Modified Base  
(B) LOCATION: 19...19  
(D) OTHER INFORMATION: Inosine

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- rec 51*
- (A) NAME/KEY: Modified Base  
(B) LOCATION: 25...25  
(D) OTHER INFORMATION: Inosine; Inosine also at position  
28

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CCGGAATTCA CANSRCANG MNWCNACNRY CAT

33

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(v) FRAGMENT TYPE:

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

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- (A) NAME/KEY: Modified Base

- (B) LOCATION: 13...13

- (D) OTHER INFORMATION: Inosine

- (A) NAME/KEY: Modified Base

- (B) LOCATION: 19...19

- (D) OTHER INFORMATION: Inosine

- (A) NAME/KEY: Modified Base

- (B) LOCATION: 25...25

- (D) OTHER INFORMATION: Inosine; Inosine also at position

28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCGGAATTCA CANSRCANM GNYGNACNRY CAT

33

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid

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(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:  
(ix) FEATURE:

(A) NAME/KEY: Modified Base  
(B) LOCATION: 13...13  
(D) OTHER INFORMATION: Inosine

15

(A) NAME/KEY:Modified Base  
(B) LOCATION: 19...19  
(D) OTHER INFORMATION: Inosine

20

(A) NAME/KEY:Modified Base  
(B) LOCATION: 25...25  
(D) OTHER INFORMATION: Inosine; Inosine also at position  
28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CCGGAATTCA CAnSCRCANM GNWCNACNMY CAT

33

25

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: cDNA  
(iii) HYPOTHETICAL: NO  
(iv) ANTISENSE: NO  
(v) FRAGMENT TYPE:  
(vi) ORIGINAL SOURCE:  
(ix) FEATURE:

35

(A) NAME/KEY: Modified Base  
(B) LOCATION: 13...13  
(D) OTHER INFORMATION: Inosine

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*MW*  
*SI*

(A) NAME/KEY:Modified Base  
 (B) LOCATION: 19...19  
 (D) OTHER INFORMATION: Inosine

5

(A) NAME/KEY:Modified Base  
 (B) LOCATION: 25...25  
 (D) OTHER INFORMATION: Inosine; Inosine also at position  
 28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

10

CCGGAATTCA CAnSRCANM GNWCNACNMY CAT

33

(2) INFORMATION FOR SEQ ID NO:11:

15

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 360 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: cDNA  
 (iii) HYPOTHETICAL: NO  
 (iv) ANTISENSE: NO  
 (v) FRAGMENT TYPE:  
 (vi) ORIGINAL SOURCE:  
 (ix) FEATURE:

25

(A) NAME/KEY: Coding Sequence  
 (B) LOCATION: 1...357  
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

30

CGG GCC AGG AGG AGG ACC CCC ACC TGT GAG CCT GCG ACC CCC TTA TGT  
 Arg Ala Arg Arg Arg Thr Pro Thr Cys Glu Pro Ala Thr Pro Leu Cys  
 1 5 10 15

48

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TGC AGG CGA GAC CAT TAC GTA GAC TTC CAG GAA CTG GGA TGG CGG GAC  
 Cys Arg Arg Asp His Tyr Val Asp Phe Gln Glu Leu Gly Trp Arg Asp  
 20 25 30

96

TGG ATA CTG CAG CCC GAG GGG TAC CAG CTG AAT TAC TGC AGT GGG CAG  
 Trp Ile Leu Gln Pro Glu Gly Tyr Gln Leu Asn Tyr Cys Ser Gly Gln  
 35 40 45

144

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	TGC CCT CCC CAC CTG GCT GGC AGC CCA GGC ATT GCT GCC TCT TTC CAT	192
	Cys Pro Pro His Leu Ala Gly Ser Pro Gly Ile Ala Ala Ser Phe His	
	50 55 60	
5	TCT GCC GTC TTC AGC CTC CTC AAA GCC AAC AAT CCT TGG CCT GCC AGT	240
	Ser Ala Val Phe Ser Leu Leu Lys Ala Asn Asn Pro Trp Pro Ala Ser	
	65 70 75 80	
	ACC TCC TGT TGT GTC CCT ACT GCC CGA AGG CCC CTC TCT CTC CTC TAC	288
	Thr Ser Cys Cys Val Pro Thr Ala Arg Arg Pro Leu Ser Leu Leu Tyr	
	85 90 95	
10	CTG GAT CAT AAT GGC AAT GTG GTC AAG ACG GAT GTG CCA GAT ATG GTG	336
	Leu Asp His Asn Gly Asn Val Val Lys Thr Asp Val Pro Asp Met Val	
	100 105 110	
	GTG GAG GCC TGT GGC TGC AGC TAG	360
15	Val Glu Ala Cys Gly Cys Ser	
	115	
	(2) INFORMATION FOR SEQ ID NO:12:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 119 amino acids	
	(B) TYPE: amino acids	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
25	(iii) HYPOTHETICAL: NO	
	(iv) ANTISENSE: NO	
	(v) FRAGMENT TYPE: internal	
	(vi) ORIGINAL SOURCE:	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
	Arg Ala Arg Arg Arg Thr Pro Thr Cys Glu Pro Ala Thr Pro Leu Cys	
	1 5 10 15	
30	Cys Arg Arg Asp His Tyr Val Asp Phe Gln Glu Leu Gly Trp Arg Asp	
	20 25 30	
	Trp Ile Leu Gln Pro Glu Gly Tyr Gln Leu Asn Tyr Cys Ser Gly Gln	
	35 40 45	
35	Cys Pro Pro His Leu Ala Gly Ser Pro Gly Ile Ala Ala Ser Phe His	
	50 55 60	

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65	Ser Ala Val Phe Ser Leu Leu Lys Ala Asn Asn Pro Trp Pro Ala Ser
	70
85	Thr Ser Cys Cys Val Pro Thr Ala Arg Arg Pro Leu Ser Leu Leu Tyr
	90
100	Leu Asp His Asn Gly Asn Val Val Lys Thr Asp Val Pro Asp Met Val
	105
115	Val Glu Ala Cys Gly Cys Ser

## (2) INFORMATION FOR SEQ ID NO:13:

- 10           (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2419 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- 15           (ii) MOLECULE TYPE: cDNA
  - (iii) HYPOTHETICAL: NO
  - (iv) ANTISENSE: NO
  - (v) FRAGMENT TYPE:
  - (vi) ORIGINAL SOURCE:
  - (ix) FEATURE:
    - (A) NAME/KEY: Coding Sequence
    - (B) LOCATION: 218...1267
    - (D) OTHER INFORMATION:
- 20

## 25           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

30	GAGCTGTGAG GGTCAAGCAC AGCTATCCAT CAGATGATCT ACTTTCAGCC TTCTTGAGTC	60
	CCAGACAATA GAAGACAGGT GGCTGTACCC TTGGCCAAGG GTAGGTGTGG CAGTGGTGTGTC	120
	TGCTGTCACT GTGCCCTCAT TGGCCCCCAG CAATCAGACT CAACAGACGG AGCAAATGCC	180
	ATCCGAGGCT CCTGAACCAG GGCCATTAC CAGGAGC ATG CGG CTC CGT GAT GTC	235
	Met Arg Leu Pro Asp Val	
	1               5	
	CAG CTC TGG CTG GTG CTG TGG GCA CTG GTG CGA GCA CAG GGG ACA	283
	Gln Leu Trp Leu Val Leu Leu Trp Ala Leu Val Arg Ala Gln Gly Thr	
	10             15             20	

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	GGG TCT GTG TGT CCC TCC TGT GGG GGC TCC AAA CTG GCA CCC CAA GCA Gly Ser Val Cys Pro Ser Cys Gly Gly Ser Lys Leu Ala Pro Gln Ala 25 30 35	331
5	GAA CGA GCT CTG GTG CTG GAG CTA GCC AAG CAG CAA ATC CTG GAT GGG Glu Arg Ala Leu Val Leu Glu Leu Ala Lys Gln Gln Ile Leu Asp Gly 40 45 50	379
	TTG CAC CTG ACC AGT CGT CCC AGA ATA ACT CAT CCT CCA CCC CAG GCA Leu His Leu Thr Ser Arg Pro Arg Ile Thr His Pro Pro Pro Gln Ala 55 60 65 70	427
10	GCG CTG ACC AGA GCC CTC CGG AGA CTA CAG CCA GGG AGT GTG GCT CCA Ala Leu Thr Arg Ala Leu Arg Arg Leu Gln Pro Gly Ser Val Ala Pro 75 80 85	475
15	GGG AAT GGG GAG GAG GTC ATC AGC TTT GCT ACT GTC ACA GAC TCC ACT Gly Asn Gly Glu Glu Val Ile Ser Phe Ala Thr Val Thr Asp Ser Thr 90 95 100	523
	TCA GCC TAC AGC TCC CTG CTC ACT TTT CAC CTG TCC ACT CCT CGG TCC Ser Ala Tyr Ser Ser Leu Leu Thr Phe His Leu Ser Thr Pro Arg Ser 105 110 115	571
20	CAC CAC CTG TAC CAT GCC CGC CTG TGG CTG CAC GTG CTC CCC ACC CTT His His Leu Tyr His Ala Arg Leu Trp Leu His Val Leu Pro Thr Leu 120 125 130	619
	CCT GGC ACT CTT TGC TTG AGG ATC TTC CGA TGG GGA CCA AGG AGG AGG Pro Gly Thr Leu Cys Leu Arg Ile Phe Arg Trp Gly Pro Arg Arg Arg 135 140 145 150	667
25	CGC CAA GGG TCC CGC ACT CTC CTG GCT GAG CAC CAC ATC ACC AAC CTG Arg Gln Gly Ser Arg Thr Leu Leu Ala Glu His His Ile Thr Asn Leu 155 160 165	715
30	GGC TGG CAT ACC TTA ACT CTG CCC TCT AGT GGC TTG AGG GGT GAG AAG Gly Trp His Thr Leu Thr Leu Pro Ser Ser Gly Leu Arg Gly Glu Lys 170 175 180	763
	TCT GGT GTC CTG AAA CTG CAA CTA GAC TGC AGA CCC CTA GAA GGC AAC Ser Gly Val Leu Lys Leu Gln Leu Asp Cys Arg Pro Leu Glu Gly Asn 185 190 195	811
35	AGC ACA GTT ACT GGA CAA CCG AGG CGG CTC TTG GAC ACA GCA GGA CAC Ser Thr Val Thr Gly Gln Pro Arg Arg Leu Leu Asp Thr Ala Gly His 200 205 210	859

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5' → 3'

5

10

5' ← 3'

20

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CAG CAG CCC TTC CTA GAG CTT AAG ATC CGA GCC AAT GAG CCT GGA GCA Gln Gln Pro Phe Leu Glu Leu Lys Ile Arg Ala Asn Glu Pro Gly Ala 215 220 225 230	907
GGC CGG GCC AGG AGG AGG ACC CCC ACC TGT GAG CCT GCG ACC CCC TTA Gly Arg Ala Arg Arg Arg Thr Pro Thr Cys Glu Pro Ala Thr Pro Leu 235 240 245	955
TGT TGC AGG CGA GAC CAT TAC GTA GAC TTC CAG GAA CTG GGA TGG CGG Cys Cys Arg Arg Asp His Tyr Val Asp Phe Gln Glu Leu Gly Trp Arg 250 255 260	1003
GAC TGG ATA CTG CAG CCC GAG GGG TAC CAG CTG AAT TAC TGC AGT GGG Asp Trp Ile Leu Gln Pro Glu Gly Tyr Gln Leu Asn Tyr Cys Ser Gly 265 270 275	1051
CAG TGC CCT CCC CAC CTG GCT GGC AGC CCA GGC ATT GCT GCC TCT TTC Gln Cys Pro Pro His Leu Ala Gly Ser Pro Gly Ile Ala Ala Ser Phe 280 285 290	1099
CAT TCT GCC GTC TTC AGC CTC CTC AAA GCC AAC AAT CCT TGG CCT GCC His Ser Ala Val Phe Ser Leu Leu Lys Ala Asn Asn Pro Trp Pro Ala 295 300 305 310	1147
AGT ACC TCC TGT GTC CCT ACT GCC CGA AGG CCC CTC TCT CTC CTC Ser Thr Ser Cys Cys Val Pro Thr Ala Arg Arg Pro Leu Ser Leu Leu 315 320 325	1195
TAC CTG GAT CAT AAT GGC AAT GTG GTC AAG ACG GAT GTG CCA GAT ATG Tyr Leu Asp His Asn Gly Asn Val Val Lys Thr Asp Val Pro Asp Met 330 335 340	1243
GTG GTG GAG GCC TGT GGC TGC AGC TAGCAAGAGG ACCTGGGGCT TTGGAGTGAA G Val Val Glu Ala Cys Gly Cys Ser 345 350	1298
AGACCAAGAT GAAAGTTCCC AGGCACAGGG CATCTGTGAC TGGAGGCATC AGATTCTGA	1358
TCCACACCCC AACCCAAACAA CCACCTGGCA ATATGACTCA CTTGACCCCT ATGGGACCCA	1418
AATGGGCACT TTCTTGTCTG AGACTCTGGC TTATTCCAGG TTGGCTGATG TGTTGGAGA	1478
TGGGTAAAGC GTTTCTTCTA AAGGGGTCTA CCCAGAAAGC ATGATTCCT GCCCTAAGTC	1538
CTGTGAGAAG ATGTCAGGGA CTAGGGAGGG AGGGAGGGAA GGCAAGAGAAA AATTACTTAG	1598
CCTCTCCCAA GATGAGAAAG TCCTCAAGTG AGGGGAGGAG GAAGCAGATA GATGGTCCAG	1658

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	CAGGCTTGAAG GCAGGGTAAG CAGGCTGGCC CAGGGTAAGG GCTGTTGAGG TACCTTAAGG	1718
	GAAGGTCAAG AGGGAGATGG GCAAGGCGCT GAGGGAGGAT GCTTAGGGGA CCCCCAGAAA	1778
	CAGGAGTCAG GAAATGAGG CACTAAGCCT AAGAAGTCC CTGGTTTTTC CCAGGGGACA	1838
	GGACCCACTG GGAGACAAGC ATTTATACTT TCTTTCTTCT TTTTATTTT TTTGAGATCG	1898
5	AGTCTCGCTC TGTCACCAGG CTGGAGTGCA GTGACACGAT CTTGGCTCAC TGCAACCTCC	1958
	GTCTCCTGGG TTCAAGTGAT TCTCTGCCT CAGCCTCCCG AGCAGCTGGG ATTACAGGCG	2018
	CCCACTAATT TTTGTATTCT TAGTAGAAC GAGGTTCAA CATGTTGCC AGGATGGTCT	2078
	CAATCTCTTG ACCTCTTGAT CCACCCGACT TGGCCTCCCG AAGTGATGAG ATTATAGGCG	2138
	TGAGCCACCG CGCCTGGCTT ATACTTTCTA AATAAAAAGG AGAAAGAAAA TCAACAAATG	2198
10	TGAGTCATAA AGAAGGGTTA GGGTGATGGT CCAGAGCAAC AGTTCTCAA GTGTACTCTG	2258
	TAGGCTTCTG GGAGGTCCCT TTTCAGGGGT GTCCACAAAG TCAAAGCTAT TTTCATAATA	2318
	ATACTAACAT GTTATTGCC TTTTGAATT TCATTACCTT AAAATTGTAT TGTGGAGTT	2378
	TCCAGAGGCC GTGTGACATG TGATTACATC ATCTTCTGA C	2419

## (2) INFORMATION FOR SEQ ID NO:14:

15	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 350 amino acids
	(B) TYPE: amino acids
	(C) STRANDEDNESS: single
	(D) TOPOLOGY: linear
20	(ii) MOLECULE TYPE: protein
	(iii) HYPOTHETICAL: NO
	(iv) ANTISENSE: NO
	(v) FRAGMENT TYPE: internal
	(vi) ORIGINAL SOURCE:
25	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Arg	Leu	Pro	Asp	Val	Gln	Leu	Trp	Leu	Val	Leu	Leu	Trp	Ala	Leu
1					5				10				15		

Val	Arg	Ala	Gln	Gly	Thr	Gly	Ser	Val	Cys	Pro	Ser	Cys	Gly	Gly	Ser
20							25					30			

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31

	Lys	Leu	Ala	Pro	Gln	Ala	Glu	Arg	Ala	Leu	Val	Leu	Glu	Leu	Ala	Lys
	35						40						45			
	Gln	Gln	Ile	Leu	Asp	Gly	Leu	His	Leu	Thr	Ser	Arg	Pro	Arg	Ile	Thr
	50						55						60			
5	His	Pro	Pro	Pro	Gln	Ala	Ala	Leu	Thr	Arg	Ala	Leu	Arg	Arg	Leu	Gln
	65						70					75				80
	Pro	Gly	Ser	Val	Ala	Pro	Gly	Asn	Gly	Glu	Glu	Val	Ile	Ser	Phe	Ala
	85									90						95
10	Thr	Val	Thr	Asp	Ser	Thr	Ser	Ala	Tyr	Ser	Ser	Leu	Leu	Thr	Phe	His
								100				105				110
	Leu	Ser	Thr	Pro	Arg	Ser	His	His	Leu	Tyr	His	Ala	Arg	Leu	Trp	Leu
	115							120					125			
	His	Val	Leu	Pro	Thr	Leu	Pro	Gly	Thr	Leu	Cys	Leu	Arg	Ile	Phe	Arg
	130						135					140				
15	Trp	Gly	Pro	Arg	Arg	Arg	Gln	Gly	Ser	Arg	Thr	Leu	Leu	Ala	Glu	
	145						150					155				160
	His	His	Ile	Thr	Asn	Leu	Gly	Trp	His	Thr	Leu	Thr	Leu	Pro	Ser	Ser
	165						170						175			
20	Gly	Leu	Arg	Gly	Glu	Lys	Ser	Gly	Val	Leu	Lys	Leu	Gln	Leu	Asp	Cys
								180			185			190		
	Arg	Pro	Leu	Glu	Gly	Asn	Ser	Thr	Val	Thr	Gly	Gln	Pro	Arg	Arg	Leu
	195							200					205			
	Leu	Asp	Thr	Ala	Gly	His	Gln	Gln	Pro	Phe	Leu	Glu	Leu	Lys	Ile	Arg
	210						215					220				
25	Ala	Asn	Glu	Pro	Gly	Ala	Gly	Arg	Ala	Arg	Arg	Arg	Thr	Pro	Thr	Cys
	225							230					235			240
	Glu	Pro	Ala	Thr	Pro	Leu	Cys	Cys	Arg	Arg	Asp	His	Tyr	Val	Asp	Phe
	245						250						255			
30	Gln	Glu	Leu	Gly	Trp	Arg	Asp	Trp	Ile	Leu	Gln	Pro	Glu	Gly	Tyr	Gln
									260			265			270	
	Leu	Asn	Tyr	Cys	Ser	Gly	Gln	Cys	Pro	Pro	His	Leu	Ala	Gly	Ser	Pro
	275							280					285			

-45-

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Gly Ile Ala Ala Ser Phe His Ser Ala Val Phe Ser Leu Leu Lys Ala  
290 295 300

Asn Asn Pro Trp Pro Ala Ser Thr Ser Cys Cys Val Pro Thr Ala Arg  
305 310 315 320

Arg Pro Leu Ser Leu Leu Tyr Leu Asp His Asn Gly Asn Val Val Lys  
325 330 335

Thr Asp Val Pro Asp Met Val Val Glu Ala Cys Gly Cys Ser  
340 345 350